

SEQUENCE LISTING

<110> Zoghbi, Huda
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Bermingham, Nessim
Hassan, Bassem

<120> COMPOSITIONS AND METHODS FOR THE THERAPEUTIC USE OF AN ATONAL-
ASSOCIATED SEQUENCE FOR DEAFNESS, OSTEOARTHRITIS, AND ABNORMAL CELL
PROLIFERATION

<130> HO-P01899US3/09906355/OTA 99-47

<140> US 09/980,381

<141> 2001-11-30

<150> US 60/137,060

<151> 1999-06-01

<150> US 60/176,993

<151> 2000-01-19

<150> PCT/US00/15410

<151> 2000-06-01

<160> 69

<170> PatentIn version 3.0

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Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
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115 120 125
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Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Gly Gln Gly Val Gln
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Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
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Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
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Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
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Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
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Arg Glu Glu Glu Asp Glu Asn Gly Leu Ser Arg Arg Arg Gly Leu Arg
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Lys Lys Lys Thr Thr Lys Leu Arg Leu Glu Arg Val Lys Phe Arg Arg
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Gln Glu Ala Asn Ala Arg Glu Arg Asn Arg Met His Gly Leu Asn Asp
 100 105 110

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Lys Leu Ser Lys Ile Glu Thr Leu Arg Leu Ala Lys Asn Tyr Ile Trp
 130 135 140

Ala Leu Ser Glu Ile Leu Arg Ile Gly Lys Arg Pro Asp Leu Leu Thr
 145 150 155 160

Phe Val Gln Asn Leu Cys Lys Gly Leu Ser Gln Pro Thr Thr Asn Leu
 165 170 175

Val Ala Gly Cys Leu Gln Leu Asn Ala Arg Ser Phe Leu Met Gly Gln
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Gly Gly Glu Ala Ala His His Thr Arg Ser Pro Tyr Ser Thr Phe Tyr
 195 200 205

Pro Pro Tyr His Ser Pro Glu Leu Ala Thr Pro Pro Gly His Gly Thr
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Leu Asp Asn Ser Lys Ser Met Lys Pro Tyr Asn Tyr Cys Ser Ala Tyr
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Glu Ser Phe Tyr Glu Ser Thr Ser Pro Glu Cys Ala Ser Pro Gln Phe
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 290 295 300
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Pro Thr Leu Gln Gly Leu Cys Thr Ala Arg Ala Ala Gln Tyr Leu Leu
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His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg Asp Glu
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Ala Asp Ser Gln Gly Glu Leu Val Arg Arg Ser Gly Cys Gly Gly Leu
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Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu Cys Lys Leu
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Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg Gln Arg Ala
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Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg Arg Leu Ala
145 150 155 160

Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn His Ala Phe
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Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp Lys Lys Leu
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Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu
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Ser Glu Leu Leu Gln Thr Pro Asn Val Gly Glu Gln Pro Pro Pro Pro
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Thr Ala Ser Cys Lys Asn Asp His His His Leu Arg Thr Ala Ser Ser
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Tyr Glu Gly Gly Ala Gly Ala Ser Ala Val Ala Gly Ala Gln Pro Ala
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Pro Gly Gly Gly Pro Arg Pro Thr Pro Pro Gly Pro Cys Arg Thr Arg
260 265 270

Phe Ser Gly Pro Ala Ser Ser Gly Gly Tyr Ser Val Gln Leu Asp Ala
275 280 285

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Leu His Phe Pro Ala Phe Glu Asp Arg Ala Leu Thr Ala Met Met Ala
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<210> 13
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<213> ZEBRA FISH

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<223> "n" can be any nucleotide

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gacaacacgg acagggagga ggaggaggag agagaggagg actataacgg gctgccaaag 180
aagaagggtc cccgcaaaaa gaaatccgag ggacgcggtg accgagtcaa aatgcgccgt 240
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<210> 14
<211> 609
<212> DNA
<213> HUMAN

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<210> 15
 <211> 675
 <212> DNA
 <213> HUMAN

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<210> 16
 <211> 1476
 <212> DNA
 <213> DROSPHILA

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<210> 17
 <211> 189
 <212> PRT
 <213> DROSOPHILA

<400> 17

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Tyr	Leu	Gly	Ser	Pro	Asn	Tyr	Asn	Leu	Thr	Gln	Leu	Pro	Pro	Val	Ser
			20				25					30			
Gly	Gln	Asp	Tyr	Gly	Gln	Gly	Ala	Phe	Leu	Ser	Pro	Glu	Trp	Gln	Phe
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Leu Asp Ala Ala Gly Gly Thr Gln Thr Glu Leu Gly Pro Ile Met Glu
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 65 70 75 80
 Ser Thr Gly Ser Asp Gly Arg Lys Ser Ser Pro Glu Gln Thr Asn Leu
 85 90 95
 Ser Pro Thr Val Gln Lys Arg Arg Arg Gln Ala Ala Asn Ala Arg Glu
 100 105 110
 Arg Lys Arg Met Asn Gly Leu Asn Ala Ala Phe Glu Arg Leu Arg Glu
 115 120 125
 Val Val Pro Ala Pro Ser Ile Asp Gln Lys Leu Ser Lys Phe Glu Thr
 130 135 140
 Leu Gln Met Ala Gln Ser Tyr Ile Leu Ala Leu Cys Asp Leu Leu Asn
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 Asn Gly Asp Val Glu Val Asp Ala Ala Ala Tyr Thr Ile Phe Gly Asp
 165 170 175
 Ser Asp Ser Gly Phe Gly Leu Ser Gly Gly Ser Leu Ser
 180 185

<210> 18
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 <212> DNA
 <213> CHICKEN

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<210> 19
 <211> 178
 <212> PRT
 <213> CHICKEN

<400> 19

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 Ala Pro Arg Glu Arg Arg Arg Arg Arg Gly Arg Ala Arg Ala Arg Thr
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 Glu Ala Leu Leu His Thr Leu Lys Arg Ser Arg Arg Val Lys Ala Asn
 35 40 45
 Asp Arg Glu Arg Asn Arg Met His His Leu Asn Ala Ala Leu Asp Glu
 50 55 60
 Leu Arg Ser Val Leu Pro Thr Phe Pro Asp Asp Thr Lys Leu Thr Lys
 65 70 75 80
 Ile Glu Thr Leu Arg Phe Ala Tyr Asn Tyr Ile Trp Ala Leu Ser Glu
 85 90 95
 Thr Leu Arg Leu Ala Glu Gln Cys Leu Pro Pro Pro Pro Ala Phe Arg
 100 105 110
 Gly Pro Pro Ala Pro Pro Ser Pro Gly Ser Asp Ala Gly Ser Trp Leu
 115 120 125
 Ser Ser Gly Ser Pro Ala Ala Pro Ser Leu Cys Ala Ser Ala Ser Gly
 130 135 140
 Pro Ser Ser Pro Ala Thr Ser Glu Asp Cys Gly Tyr Val Pro Ser Asp
 145 150 155 160
 Ala Leu Arg Ala Phe Arg Gly Leu Pro Pro Ala Ala Pro Gly Ala Pro
 165 170 175

Cys Arg

<210> 20
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 <212> DNA
 <213> CHICKEN

<400> 20
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<210> 21
 <211> 213
 <212> PRT
 <213> CHICKEN

<400> 21

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			20					25					30		
Ser	Ala	Gly	Glu	Glu	Asp	Glu	Asp	Glu	Glu	Asp	Gly	Arg	Pro	Arg	Arg
		35					40					45			
Leu	Gln	Glu	Gly	Ala	Arg	Arg	Ala	Gly	Arg	Gln	Arg	Gly	Pro	Pro	Arg
	50					55					60				
Ala	Ala	Arg	Thr	Ala	Glu	Thr	Ala	Gln	Arg	Ile	Lys	Arg	Ser	Arg	Arg
65					70				75					80	
Leu	Lys	Ala	Asn	Asn	Arg	Glu	Arg	Asn	Arg	Met	His	Asn	Leu	Asn	Ala
			85					90						95	
Ala	Leu	Asp	Ala	Leu	Arg	Asp	Val	Leu	Pro	Thr	Phe	Pro	Glu	Asp	Ala
		100						105					110		
Lys	Leu	Thr	Lys	Ile	Glu	Thr	Leu	Arg	Phe	Ala	His	Asn	Tyr	Ile	Trp
	115						120					125			
Ala	Leu	Thr	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Ala	Ala	Arg	Leu	Gly	Gly
	130					135					140				

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Ala Ala Asp Ala Ala Pro Gly Ala Ala Ala Glu Gly Ser Pro Ser Pro
 145 150 155 160

Ala Ser Ser Trp Ser Gly Gly Ala Ser Pro Ala Pro Ser Ala Ser Pro
 165 170 175

Tyr Ala Cys Thr Leu Ser Pro Gly Ser Pro Ala Gly Ser Ala Ser Asp
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Ala Glu His Trp Pro Pro Pro Arg Gly Arg Phe Ala Pro Pro Pro Pro
 195 200 205

Pro His Arg Cys Leu
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<210> 22
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<210> 23
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 <212> PRT
 <213> MOUSE

<400> 23

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Pro Gly Arg Leu Glu Ser Ala Ala Arg Arg Arg Leu Ala Ala Asn Ala
 35 40 45

Arg Glu Arg Arg Arg Met Gln Gly Leu Asn Thr Ala Phe Asp Arg Leu
 50 55 60

Arg Arg Val Val Pro Gln Trp Gly Gln Asp Lys Lys Leu Ser Lys Tyr
 65 70 75 80

Glu Thr Leu Gln Met Ala Leu Ser Tyr Ile Ile Ala Leu Thr Arg Ile

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Leu Ala Glu Ala Glu Arg Asp Trp Val Gly Leu Arg Cys Glu Gln Arg
 100 105 110

Gly Arg Asp His Pro Tyr Leu Pro Phe Pro Gly Ala Arg Leu Gln Val
 115 120 125

Asp Pro Glu Pro Tyr Gly Gln Arg Leu Phe Gly Phe Gln Pro Glu Pro
 130 135 140

Phe Pro Met Ala Ser
 145

<210> 24
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 <212> DNA
 <213> MOUSE

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<210> 25
 <211> 214
 <212> PRT
 <213> MOUSE

<400> 25

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 1 5 10 15

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Thr Gln Gln Pro Phe Pro Gly Ala Ser Asp His Glu Val Leu Ser Ser
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 Asn Ser Thr Pro Pro Ser Pro Thr Leu Ile Pro Arg Asp Cys Ser Glu
 35 40 45
 Ala Glu Val Gly Asp Cys Arg Gly Thr Ser Arg Lys Leu Arg Ala Arg
 50 55 60
 Arg Gly Gly Arg Asn Arg Pro Lys Ser Glu Leu Ala Leu Ser Lys Gln
 65 70 75 80
 Arg Arg Ser Arg Arg Lys Lys Ala Asn Asp Arg Glu Arg Asn Arg Met
 85 90 95
 His Asn Leu Asn Ser Ala Leu Asp Ala Leu Arg Gly Val Leu Pro Thr
 100 105 110
 Phe Pro Asp Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala
 115 120 125
 His Asn Tyr Ile Trp Ala Leu Thr Gln Thr Leu Arg Ile Ala Asp His
 130 135 140
 Ser Phe Tyr Gly Pro Glu Pro Pro Val Pro Cys Gly Glu Leu Gly Ser
 145 150 155 160
 Pro Gly Gly Gly Ser Asn Gly Asp Trp Gly Ser Ile Tyr Ser Pro Val
 165 170 175
 Ser Gln Ala Gly Asn Leu Ser Pro Thr Ala Ser Leu Glu Glu Phe Pro
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<210> 26
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<400> 26
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<210> 27
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<400> 27

Met His Gly Leu Asn Ala Ala Leu Asp Asn Pro Arg Lys Val Val Pro
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Cys Tyr Ser Lys Thr Gln Lys Leu

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<210> 28
 <211> 66
 <212> DNA
 <213> MOUSE

<400> 28
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<210> 29
 <211> 22
 <212> PRT
 <213> MOUSE

<400> 29

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Cys Tyr Ser Lys Thr Gln
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<210> 30
 <211> 1385
 <212> DNA
 <213> MOUSE

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<210> 31
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 <212> PRT
 <213> MOUSE

<400> 31

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 35 40 45
 Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Glu Gln Gly Val Gln
 50 55 60
 Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
 65 70 75 80
 Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
 85 90 95
 Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr
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 Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
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 Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
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 Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
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 Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
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 Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser

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Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp		
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Tyr Trp Gln Pro Pro Pro Glu Lys His Arg Tyr Ala Pro His Leu		
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35 40 45

Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Asp Gly
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Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala
65 70 75 80

Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu
85 90 95

Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg
100 105 110

Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr
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Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu
130 135 140

Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys
145 150 155 160

Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu
165 170 175

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 180 185 190
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 195 200 205
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 210 215 220
 Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro
 225 230 235 240
 Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu
 245 250 255
 Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu
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 Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser
 275 280 285
 Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr
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Arg Arg Arg Met Gln Gly Leu Asn Thr Ala Phe Asp Arg Leu Arg Lys
50 55 60
Val Val Pro Gln Trp Gly Gln Asp Lys Lys Leu Ser Lys Tyr Glu Thr
65 70 75 80
Leu Gln Met Ala Leu Ser Tyr Ile Met Ala Leu Thr Arg Ile Leu Ala
85 90 95
Glu Ala Glu Arg Tyr Ser Thr Glu Arg Glu Trp Ile Asn Leu His Cys
100 105 110
Glu His Phe His Pro Glu Ser Tyr His His Tyr Thr Gly Gln Lys Val
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Gly Ser Ala Arg Gly Gln Arg Gly Ala Glu Ala Gly Gln Gly Val Gln
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Gly Ser Pro Ala Ser Gly Ala Gly Gly Cys Arg Pro Gly Arg Leu Leu
65      70      75      80

Gly Leu Met His Glu Cys Lys Arg Arg Pro Ser Arg Ser Arg Ala Val
      85      90      95

Ser Arg Gly Ala Lys Thr Ala Glu Thr Val Gln Arg Ile Lys Lys Thr
      100     105     110

Arg Arg Leu Lys Ala Asn Asn Arg Glu Arg Asn Arg Met His Asn Leu
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Asn Ala Ala Leu Asp Ala Leu Arg Glu Val Leu Pro Thr Phe Pro Glu
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Asp Ala Lys Leu Thr Lys Ile Glu Thr Leu Arg Phe Ala His Asn Tyr
145      150      155      160

Ile Trp Ala Leu Thr Glu Thr Leu Arg Leu Ala Asp His Cys Ala Gly
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Ala Gly Gly Leu Gln Gly Ala Leu Phe Thr Glu Ala Val Leu Leu Ser
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Pro Gly Ala Ala Leu Gly Ala Ser Gly Asp Ser Pro Ser Pro Pro Ser
      195     200     205

Ser Trp Ser Cys Thr Asn Ser Pro Ala Ser Ser Ser Asn Ser Thr Ser
      210     215     220

Pro Tyr Ser Cys Thr Leu Ser Pro Ala Ser Pro Gly Ser Asp Val Asp
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Pro Leu Ala Arg Asp Cys Ile
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Tyr	Asn	Tyr	Gln	Ser	Pro	Gly	Leu	Pro	Ser	Pro	Pro	Tyr	Gly	Asn	Ile
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Asp	Val	His	His	Leu	His	Leu	Lys	Pro	Ser	Ser	Phe	Lys	Pro	Val	Met
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Asp	Pro	Ser	Val	Val	Thr	His	Thr	Leu	Asn	Cys	Thr	Thr	Pro	Pro	Tyr

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Lys Gln Asp Ser Ser Pro Asp Met Asp Lys Ser Tyr Ala Phe Arg Ser
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Pro Tyr Pro Ala Leu Gly Leu Gly Gly Ser His Gly His Ala Ser His
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Phe His Thr Ser Val Pro Arg Tyr Glu Leu Pro Ile Asp Met Ala Tyr
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Glu Pro Tyr Pro His His Ala Ile Phe Thr Glu
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taaacagtgg tcattcacct cccactctaa ttaaggcaaa gcagatgctt gtgggctgag	1140

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<210> 44
 <211> 337
 <212> PRT
 <213> MOUSE

<400> 44

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			20					25					30		
Lys	Pro	Glu	Ser	Phe	Pro	Lys	Gln	Val	Val	Leu	Arg	Gly	Lys	Ser	Ile
			35				40					45			
Lys	Arg	Ala	Pro	Gly	Glu	Glu	Thr	Glu	Lys	Glu	Glu	Glu	Glu	Glu	Asp
	50					55				60					
Arg	Glu	Glu	Glu	Asp	Glu	Asn	Gly	Leu	Ser	Arg	Arg	Arg	Gly	Leu	Arg
65					70				75					80	
Lys	Lys	Lys	Thr	Thr	Lys	Leu	Arg	Leu	Glu	Arg	Val	Lys	Phe	Arg	Arg
			85					90					95		
Gln	Glu	Ala	Asn	Ala	Arg	Glu	Arg	Asn	Arg	Met	His	Gly	Leu	Asn	Asp
			100					105					110		
Ala	Leu	Asp	Asn	Leu	Arg	Lys	Val	Val	Pro	Cys	Tyr	Ser	Lys	Thr	Gln
		115					120					125			
Lys	Leu	Ser	Lys	Ile	Glu	Thr	Leu	Arg	Leu	Ala	Lys	Asn	Tyr	Ile	Trp
	130					135					140				
Ala	Leu	Ser	Glu	Ile	Leu	Arg	Ile	Gly	Lys	Arg	Pro	Asp	Leu	Leu	Thr
145					150				155						160
Phe	Val	Gln	Asn	Leu	Cys	Lys	Gly	Leu	Ser	Gln	Pro	Thr	Thr	Asn	Leu
				165					170					175	
Val	Ala	Gly	Cys	Leu	Gln	Leu	Asn	Ala	Arg	Ser	Phe	Leu	Met	Gly	Gln
			180					185					190		
Gly	Gly	Glu	Ala	Ala	His	His	Thr	Arg	Ser	Pro	Tyr	Ser	Thr	Phe	Tyr
		195					200					205			

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Pro 210	Pro	Tyr	His	Ser	Pro	Glu 215	Leu	Ala	Thr	Pro	Pro 220	Gly	His	Gly	Thr
Leu 225	Asp	Asn	Ser	Lys	Ser 230	Met	Lys	Pro	Tyr	Asn 235	Tyr	Cys	Ser	Ala	Tyr 240
Glu	Ser	Phe	Tyr	Glu 245	Ser	Thr	Ser	Pro	Glu 250	Cys	Ala	Ser	Pro	Gln 255	Phe
Glu	Gly	Pro	Leu 260	Ser	Pro	Pro	Pro	Ile 265	Asn	Tyr	Asn	Gly	Ile 270	Phe	Ser
Leu	Lys	Gln 275	Glu	Glu	Thr	Leu	Asp 280	Tyr	Gly	Lys	Asn	Tyr 285	Asn	Tyr	Gly
Met 290	His	Tyr	Cys	Ala	Val	Pro 295	Pro	Arg	Gly	Pro	Leu 300	Gly	Gln	Gly	Ala
Met 305	Phe	Arg	Leu	Pro	Thr 310	Asp	Ser	His	Phe	Pro 315	Tyr	Asp	Leu	His	Leu 320
Arg	Ser	Gln	Ser	Leu 325	Thr	Met	Gln	Asp 330	Glu	Leu	Asn	Ala	Val	Phe 335	His

Asn

<210>	45
<211>	1393
<212>	DNA
<213>	MOUSE

<400>	45						
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gccattgcag	tgcgatgtcc	cgcttctgtc	atgcagaaga	gtgggctgag	gtaaaagagt		240
tgggggacca	ccatcgccat	ccccagccgc	accacgtccc	gccgctgacg	ccacagccac		300
ctgctaccct	gcaggcgaga	gaccttcccg	tctaccgggc	agaactgtcc	ctcctggata		360
gcaccgaccc	acgcgcctgg	ctgactccca	ctttgcaggg	cctctgcacg	gcacgcgccg		420
cccagtatct	gctgcattct	cccgagctgg	gtgcctccga	ggccgcggcg	ccccggggacg		480
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ccggggcccg	caaagtacgg	gaacagctgt	gcaagctgaa	gggtgggggtt	gtagtggacg		600
agcttggctg	cagccgccag	cgagcccctt	ccagcaaaca	ggtgaatggg	gtacagaagc		660
aaaggaggct	ggcagcaaac	gcaaggggaac	ggcgcaggat	gcacgggctg	aaccacgcct		720
tcgaccagct	gcgcaacgtt	atcccgtcct	tcaacaacga	caagaagctg	tccaaatatg		780
agaccctaca	gatggcccag	atctacatca	acgtctgttc	ggagttgctg	cagactccca		840

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gagagttttc ccccccactct cattacagtg actctgatga ggccagttag gaaggcaaca 1260
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cggacggctg cag 1393

<210> 46
<211> 351
<212> PRT
<213> MOUSE

<400> 46

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			20					25						30	
Pro	Gln	Pro	Pro	Ala	Thr	Leu	Gln	Ala	Arg	Asp	Leu	Pro	Val	Tyr	Pro
			35				40						45		
Ala	Glu	Leu	Ser	Leu	Leu	Asp	Ser	Thr	Asp	Pro	Arg	Ala	Trp	Leu	Thr
			50			55					60				
Pro	Thr	Leu	Gln	Gly	Leu	Cys	Thr	Ala	Arg	Ala	Ala	Gln	Tyr	Leu	Leu
65					70				75					80	
His	Ser	Pro	Glu	Leu	Gly	Ala	Ser	Glu	Ala	Ala	Ala	Pro	Arg	Asp	Glu
			85					90						95	
Ala	Asp	Ser	Gln	Gly	Glu	Leu	Val	Arg	Arg	Ser	Gly	Cys	Gly	Gly	Leu
			100					105					110		
Ser	Lys	Ser	Pro	Gly	Pro	Val	Lys	Val	Arg	Glu	Gln	Leu	Cys	Lys	Leu
			115				120					125			
Lys	Gly	Gly	Val	Val	Val	Asp	Glu	Leu	Gly	Cys	Ser	Arg	Gln	Arg	Ala
			130			135					140				
Pro	Ser	Ser	Lys	Gln	Val	Asn	Gly	Val	Gln	Lys	Gln	Arg	Arg	Leu	Ala
145					150					155				160	
Ala	Asn	Ala	Arg	Glu	Arg	Arg	Arg	Met	His	Gly	Leu	Asn	His	Ala	Phe
				165					170					175	

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Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp Lys Lys Leu
 180 185 190
 Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile Asn Ala Leu
 195 200 205
 Ser Glu Leu Leu Gln Thr Pro Asn Val Gly Glu Gln Pro Pro Pro Pro
 210 215 220
 Thr Ala Ser Cys Lys Asn Asp His His His Leu Arg Thr Ala Ser Ser
 225 230 235 240
 Tyr Glu Gly Gly Ala Gly Ala Ser Ala Val Ala Gly Ala Gln Pro Ala
 245 250 255
 Pro Gly Gly Gly Pro Arg Pro Thr Pro Pro Gly Pro Cys Arg Thr Arg
 260 265 270
 Phe Ser Gly Pro Ala Ser Ser Gly Gly Tyr Ser Val Gln Leu Asp Ala
 275 280 285
 Leu His Phe Pro Ala Phe Glu Asp Arg Ala Leu Thr Ala Met Met Ala
 290 295 300
 Gln Lys Asp Leu Ser Pro Ser Leu Pro Gly Gly Ile Leu Gln Pro Val
 305 310 315 320
 Gln Glu Asp Asn Ser Lys Thr Ser Pro Arg Ser His Arg Ser Asp Gly
 325 330 335
 Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu Ala Ser
 340 345 350

<210> 47
 <211> 993
 <212> DNA
 <213> MOUSE

<400> 47
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 tatggaatgc tcggaacctt aactgaagag catgacagta ttgaggagga tgaagaagag 180
 gaagaagatg gagataaacc taaaagaaga ggtcccaaga aaaagaagat gactaaagct 240
 cgccttgaaa gattcagggc tcgaagagtc aaggccaatg ctagagaacg gaccgggatg 300
 catggcctga atgatgcctt ggataatctt aggagagtca tgccatgtta ctctaaaact 360
 caaaagcttt ccaagataga gactcttcga ctggcaagga actacatctg ggccttgtct 420
 gaagtccctgg agactggtca gacacttgaa gggaagggat ttgtagagat gctatgtaaa 480
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 accctcctgg agaagcatga ggaaaaatct tcaatttgtg actctactat ctctgtccac 600
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aacttctcct taaagcaaga cggctcccct gatttgga aaacctacaa tttcatgcca 840
cattatacct ctgcaagtct aagttcaggg catgtgcatt caactccctt tcagactggc 900
actccccgct atgatgttcc tgtagacctg agctatgatt cctactccca ccatagcatt 960
ggaactcagc tcaatacgat cttctctgat tag 993

<210> 48
<211> 330
<212> PRT
<213> MOUSE

<400> 48

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Glu Gln Glu Arg Arg Pro Gly Ser Tyr Gly Met Leu Gly Thr Leu Thr
35 40 45
Glu Glu His Asp Ser Ile Glu Glu Asp Glu Glu Glu Glu Asp Gly
50 55 60
Asp Lys Pro Lys Arg Arg Gly Pro Lys Lys Lys Lys Met Thr Lys Ala
65 70 75 80
Arg Leu Glu Arg Phe Arg Ala Arg Arg Val Lys Ala Asn Ala Arg Glu
85 90 95
Arg Thr Arg Met His Gly Leu Asn Asp Ala Leu Asp Asn Leu Arg Arg
100 105 110
Val Met Pro Cys Tyr Ser Lys Thr Gln Lys Leu Ser Lys Ile Glu Thr
115 120 125
Leu Arg Leu Ala Arg Asn Tyr Ile Trp Ala Leu Ser Glu Val Leu Glu
130 135 140
Thr Gly Gln Thr Leu Glu Gly Lys Gly Phe Val Glu Met Leu Cys Lys
145 150 155 160
Gly Leu Ser Gln Pro Thr Ser Asn Leu Val Ala Gly Cys Leu Gln Leu
165 170 175
Gly Pro Gln Ser Thr Leu Leu Glu Lys His Glu Glu Lys Ser Ser Ile
180 185 190
Cys Asp Ser Thr Ile Ser Val His Ser Phe Asn Tyr Gln Ser Pro Gly
195 200 205
Leu Pro Ser Pro Pro Tyr Gly His Met Glu Thr His Ser Leu His Leu
210 215 220

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Lys Pro Gln Pro Phe Lys Ser Leu Gly Asp Ser Phe Gly Ser His Pro
 225 230 235 240
 Pro Asp Cys Ser Thr Pro Pro Tyr Glu Gly Pro Leu Thr Pro Pro Leu
 245 250 255
 Ser Ile Ser Gly Asn Phe Ser Leu Lys Gln Asp Gly Ser Pro Asp Leu
 260 265 270
 Glu Lys Ser Tyr Asn Phe Met Pro His Tyr Thr Ser Ala Ser Leu Ser
 275 280 285
 Ser Gly His Val His Ser Thr Pro Phe Gln Thr Gly Thr Pro Arg Tyr
 290 295 300
 Asp Val Pro Val Asp Leu Ser Tyr Asp Ser Tyr Ser His His Ser Ile
 305 310 315 320
 Gly Thr Gln Leu Asn Thr Ile Phe Ser Asp
 325 330

<210> 49
 <211> 2264
 <212> DNA
 <213> FROG

<400> 49
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 cctgtcttgt agctggagag ctttgtatcg atgctaagag cactgggtat ctacaaagag 120
 gatcactgca tatgaatgga ataaggagtg ctgctgctac ccaggctggg gtttgttccg 180
 agcccttcaa aaccttttgg ccatagaatc actgtgttga catgaagtca gattcaccag 240
 tgcatgggga gtcccatact gaatgccagt caccatgccc actaagttgc atgccagcca 300
 ggctggaagg ctctaccaag agacgtctgg ctgccaatgc cagggaaaga aggagaatgc 360
 aaggactgaa taccgccttc gatagtctga ggaaagttgt accgcaatgg ggtgaggaca 420
 aaaaactttc caagtatgag actctacaga tggcactgag ctacatcatg gcactaagca 480
 ggatcctcac ggaagcagaa agatacagca gaactgatcc aggggaatgg actaaaatgc 540
 actttgatca cattcaggaa gaacagtgcc tcagttatat gggagtgaga tgcccaagag 600
 actgtgatcg ctacctgccc cagacttttt ctactagga taggagatgt gagcaacagt 660
 cagcaggcaa ggtactatag acctgaagat agcagtgtat tcctacacac agcagccaat 720
 aatacaggga catttgcac atgggttatt tgtcatgtca ttctgcccaa tgcaactgctt 780
 atttcattaa gcacccaaag tcccaggact gggaatatat gtagggcacc ccacgtgatg 840
 cagcccaaag tatgtgctgc tgcaactgat agtgagctgt gggacactgg aaaagcaaag 900
 tgcgctggta ttttgtaa atgaaaatgtca ttatgggtgg catataataa ttacttacac 960
 acagcacagt tatataattt cattgctgtt agaaagcccc tttgtctctt acccccac 1020

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Met	Lys	Ser	Asp	Ser	Pro	Val	His	Gly	Glu	Ser	His	Thr	Glu	Cys	Gln	
1				5					10					15		
	Ser	Pro	Cys	Pro	Leu	Ser	Cys	Met	Pro	Ala	Arg	Leu	Glu	Gly	Ser	Thr
				20					25					30		
	Lys	Arg	Arg	Leu	Ala	Ala	Asn	Ala	Arg	Glu	Arg	Arg	Arg	Met	Gln	Gly
				35				40					45			
	Leu	Asn	Thr	Ala	Phe	Asp	Ser	Leu	Arg	Lys	Val	Val	Pro	Gln	Trp	Gly

50

55

60

Glu Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser
65 70 75 80

Tyr Ile Met Ala Leu Ser Arg Ile Leu Thr Glu Ala Glu Arg Tyr Ser
85 90 95

Arg Thr Asp Pro Gly Glu Trp Thr Lys Met His Phe Asp His Ile Gln
100 105 110

Glu Glu Gln Cys Leu Ser Tyr Met Gly Val Arg Cys Pro Arg Asp Cys
115 120 125

Asp Arg Tyr Leu Pro Gln Thr Phe Ser His
130 135

<210> 51

<211> 2123

<212> DNA

<213> FROG

<400> 51

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taaaaatgaa ataaggagat actaccagg ctgggggtta ttttgagtct ttcagaactt 180
tctagggata gaatatctct gctgacatga agtcagattc accagtgcac agggagtccc 240
atactggatg ccagtcacca tgcccactaa ggtgcttgcc agccaggctg gaaggctcta 300
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ccttcgatag tctgaggaaa gttgtaccac aatggggtga agacaaacaa ctttccaaat 420
atgagactct gcagatggcg ctgagctaca tcatggcact gagcaggatc ctctcggaag 480
cagagaggta cagcaggact gatccagagg aatggactaa tattcaatat gatcacattg 540
aggaggagca gtgcctcagt tatatggagg tgagatgcc aagagactgt gatcgttacc 600
tgccccagac tttttctcac taggataaga gcaggcaagg tactactgac ctgaagacag 660
cactgtttta atataatggg tcggttatac agcacccaat gatacaggga catttgcac 720
atgggctatt tgtcatgttg tttttcccaa tgcaatgctt atttccttaa gcaccctacg 780
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gtcactactt tccatgttac ttatgcactg ttatcagata acatagagaa agtagtat 1080
atacattaga aaaagtacta tatgtgcata taaattggcg tttaaagcag tctggataaa 1140

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aggcactgct cataagggaa aggaaacatt tttgtcactt gctgataata caaattgcat 1260
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caatgtactg tatacatgct gacctataag ggctatgtag caaagttggg aaaaagtttt 1740
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tgaaaacatt actagcccct tgccaatgta ttcttatctg tcaaattcag gagttcatga 1920
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<210> 52
<211> 138
<212> PRT
<213> FROG

<400> 52

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Ser Pro Cys Pro Leu Arg Cys Leu Pro Ala Arg Leu Glu Gly Ser Thr
20 25 30

Lys Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Gly
35 40 45

Leu Asn Thr Ala Phe Asp Ser Leu Arg Lys Val Val Pro Gln Trp Gly
50 55 60

Glu Asp Lys Gln Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Leu Ser
65 70 75 80

Tyr Ile Met Ala Leu Ser Arg Ile Leu Ser Glu Ala Glu Arg Tyr Ser
85 90 95

Arg Thr Asp Pro Glu Glu Trp Thr Asn Ile Gln Tyr Asp His Ile Glu

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100 105 110

Glu Glu Gln Cys Leu Ser Tyr Met Glu Val Arg Cys Pro Arg Asp Cys
115 120 125

Asp Arg Tyr Leu Pro Gln Thr Phe Ser His
130 135

<210> 53
<211> 136
<212> DNA
<213> BEETLE

<400> 53
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agacaagtta taccaagctt ggacgctgac cacaaattga gcaagtttga gactctgcag 120
atggcccaga cctaca 136

<210> 54
<211> 45
<212> PRT
<213> BEETLE

<400> 54

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Gly Leu Asn Glu Ala
1 5 10 15

Phe Asp Arg Leu Arg Gln Val Ile Pro Ser Leu Asp Ala Asp His Lys
20 25 30

Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr
35 40 45

<210> 55
<211> 137
<212> DNA
<213> BEETLE

<400> 55
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cgggacgtgg tgccgtccct tgggaacgat cggaagctgt ccaagtttga gacacttcag 120
atggcccaga cctacat 137

<210> 56
<211> 45
<212> PRT
<213> BEETLE

<400> 56

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Asn Ser Leu Asn Asp Ala
1 5 10 15

Phe Asp Arg Leu Arg Asp Val Val Pro Ser Leu Gly Asn Asp Arg Lys

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Leu Ser Lys Phe Glu Thr Leu Gln Met Ala Gln Thr Tyr
 35 40 45

<210> 57
 <211> 1572
 <212> DNA
 <213> HUMAN

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 <223> "n" can be any nucleotide

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 <223> "n" can be any nucleotide

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 <222> (1564)..(1564)
 <223> "n" can be any nucleotide

<400> 57
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 ggagaggagc ggggggagac tgagtggcgc gtgccgcttt ttaaaggggc gcagcgcctt 180
 cagcaaccgg agaagcatag ttgcacgcga cctggtgtgt gatctccgag tgggtggggg 240
 agggctcagg agggaaaaaa aaataagacg ttgcagaaga gacccggaaa gggccttttt 300
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tgggctgcag ccgccaacgg gcccttcca gcaaacaggt gaatggggtg cagaagcaga 840
 gacggctagc agccaacgcc agggagcggc gcaggatgca tgggctgaac cacgccttcg 900
 accagctgcg caatgttatc ccgtcgttca acaacgacaa gaagctgtcc aaatatgaga 960
 ccctgcagat ggcccaaata tacatcaacg ctttgtccga gctgctacaa acgcccagcg 1020
 gaggggaaca gccaccgccc cctccagcct cctgcaaaag cgaccaccac caccttcgca 1080
 ccgcggcctc ctatgaaggg ggcgcgggca acgcgaccgc agctgggggt cagcaggctt 1140
 ccggagggag ccageggccg accccgcccg ggagttgccg gactcgcttc tcagccccag 1200
 cttctgcggg agggtagctg gtgcagctgg acgctctgca cttctcgact ttcgaggaca 1260
 gcgccttgac agcgatgatg gcgcaaaaga atttgtctcc ttctctcccc gggagcatct 1320
 tgcagccagt gcaggaggaa aacagcaaaa cttcgccctg gtcccacaga agcgacgggg 1380
 aattttcccc ccattcccat tacagtgact cggatgaggc aagttaggaa ggtgacagaa 1440
 gcctgaaaac tgagacagaa acaaaactgc cttttcccag tgcgcgggaa gccccnggt 1500
 taangatccc cgcacccttt aatttnggt ctgcgatggt cgttgtttag caacgacttg 1560
 gctncagatg gt 1572

<210> 58
 <211> 354
 <212> PRT
 <213> HUMAN

<400> 58

Met Ser Arg Leu Leu His Ala Glu Glu Trp Ala Glu Val Lys Glu Leu
 1 5 10 15
 Gly Asp His His Arg Gln Pro Gln Pro His His Leu Pro Gln Pro Pro
 20 25 30
 Pro Pro Pro Gln Pro Pro Ala Thr Leu Gln Ala Arg Glu His Pro Val
 35 40 45
 Tyr Pro Pro Glu Leu Ser Leu Leu Asp Ser Thr Asp Pro Arg Ala Trp
 50 55 60
 Leu Ala Pro Thr Leu Gln Gly Ile Cys Thr Ala Arg Ala Ala Gln Tyr
 65 70 75 80
 Leu Leu His Ser Pro Glu Leu Gly Ala Ser Glu Ala Ala Ala Pro Arg
 85 90 95
 Asp Glu Val Asp Gly Arg Gly Glu Leu Val Arg Arg Ser Ser Gly Gly
 100 105 110
 Ala Ser Ser Ser Lys Ser Pro Gly Pro Val Lys Val Arg Glu Gln Leu
 115 120 125
 Cys Lys Leu Lys Gly Gly Val Val Val Asp Glu Leu Gly Cys Ser Arg

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130

135

140

Gln Arg Ala Pro Ser Ser Lys Gln Val Asn Gly Val Gln Lys Gln Arg
145 150 155 160

Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn
165 170 175

His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp
180 185 190

Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
195 200 205

Asn Ala Leu Ser Glu Leu Leu Gln Thr Pro Ser Gly Gly Glu Gln Pro
210 215 220

Pro Pro Pro Pro Ala Ser Cys Lys Ser Asp His His His Leu Arg Thr
225 230 235 240

Ala Ala Ser Tyr Glu Gly Gly Ala Gly Asn Ala Thr Ala Ala Gly Ala
245 250 255

Gln Gln Ala Ser Gly Gly Ser Gln Arg Pro Thr Pro Pro Gly Ser Cys
260 265 270

Arg Thr Arg Phe Ser Ala Pro Ala Ser Ala Gly Gly Tyr Ser Val Gln
275 280 285

Leu Asp Ala Leu His Phe Ser Thr Phe Glu Asp Ser Ala Leu Thr Ala
290 295 300

Met Met Ala Gln Lys Asn Leu Ser Pro Ser Leu Pro Gly Ser Ile Leu
305 310 315 320

Gln Pro Val Gln Glu Glu Asn Ser Lys Thr Ser Pro Arg Ser His Arg
325 330 335

Ser Asp Gly Glu Phe Ser Pro His Ser His Tyr Ser Asp Ser Asp Glu
340 345 350

Ala Ser

<210> 59

<211> 485

<212> DNA

<213> CHICKEN

<220>

<221> misc_feature

<222> (147)..(147)

<223> "n" can be any nucleotide

<400> 59

ccgctgctgg ggccggacgg ggcggctgcg gcttcgcccc cggctggctg ggcgtgtgct 60

gcgccgcacg cgtgcccgcg gcgtcgccgc gctacctgct gcccgccgac gaggaggacg 120

aggcggcccc tggcgggggg cgcggcncgc gttccggcgg gagcagcccc gggggagcgc 180

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ggggcgggcg cgggcgcgcg gggcgggcg gcggggggcg ggccgcgggc gcaggtgagc 240
 ggcgtgcaga agcagcggcg gctggcggcc aacgcgcggg agcgggcgcg gatgcacggg 300
 ctgaaccacg ccttcgacca gctgcgtaat gtcatcccct ccttcaacaa cgacaagaag 360
 ctctccaagt acgagacgct gcagatggcg caaatctaca tcagcgccct cgccgagctg 420
 ctgcacgggc cgcccgcgcc ccccgagccg cccgccaagg ccgagctccg cggggccccc 480
 ttcga 485

<210> 60
 <211> 161
 <212> PRT
 <213> CHICKEN

<400> 60

Pro Leu Leu Gly Pro Asp Gly Ala Ala Ala Ala Ser Pro Pro Ala Gly
 1 5 10 15
 Trp Ala Cys Ala Ala Pro His Ala Cys Pro Pro Arg Arg Arg Ala Thr
 20 25 30
 Cys Cys Pro Pro Thr Arg Arg Thr Arg Arg Pro Val Ala Gly Gly Ala
 35 40 45
 Ala Arg Val Pro Ala Gly Ala Ala Pro Gly Glu Arg Gly Ala Ala Ala
 50 55 60
 Gly Ala Arg Gly Gly Gly Gly Gly Ala Gly Pro Arg Ala Gln Val Ser
 65 70 75 80
 Gly Val Gln Lys Gln Arg Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg
 85 90 95
 Arg Met His Gly Leu Asn His Ala Phe Asp Gln Leu Arg Asn Val Ile
 100 105 110
 Pro Ser Phe Asn Asn Asp Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln
 115 120 125
 Met Ala Gln Ile Tyr Ile Ser Ala Leu Ala Glu Leu Leu His Gly Pro
 130 135 140
 Pro Ala Pro Pro Glu Pro Pro Ala Lys Ala Glu Leu Arg Gly Ala Pro
 145 150 155 160

Phe

<210> 61
 <211> 138
 <212> DNA
 <213> PUFFER FISH

<400> 61

gcggcgaacg cgagggagag gaggagaatg cacggcctga ataaagcgtt tgacgaactg 60

aggagcgtca ttccttcctt ggaaaatgag agaaagctct ccaagtatga cactctccag 120
 atggcccaaa cctacatc 138

<210> 62
 <211> 46
 <212> PRT
 <213> PUFFER FISH

<400> 62

Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn Lys Ala
 1 5 10 15

Phe Asp Glu Leu Arg Ser Val Ile Pro Ser Leu Glu Asn Glu Arg Lys
 20 25 30

Leu Ser Lys Tyr Asp Thr Leu Gln Met Ala Gln Thr Tyr Ile
 35 40 45

<210> 63
 <211> 1477
 <212> DNA
 <213> DROSOPHILA

<400> 63

atcatcttgt tagcggcttt agagccgaat cgttttctag cgccatttta agctcgcaac 60
 gaactgaggt ataaccgggc tctctgagac cgctgcaact caccaccaac tgccattggt 120
 cgtgccactc gggcggcacg tgctgccttc tgtggcaact cgtttacctg cccccctacc 180
 tgcctttcag gccctttctga ccgtcgtggt ggatttgtga gtataaatag ggccgaaagg 240
 acgagagacc agtcagaaac ccgccagcac tcgcagcggt cgtatcgttt catccagcaa 300
 cataacacca ccatacagca gcagcaacat gtcgtccagt gagatctatc gctactacta 360
 caagacctcc gaggacttgc agggcttcaa gacagccgcc gccgagccgt acttcaatcc 420
 catggcagcc tacaatcccg gcgtgaccca ctaccagttc aatggcaaca ccctggccag 480
 cagcagcaac tacttgtcgg ccaatggctt catcagcttc gagcaggcca gttccgatgg 540
 ctggatctcc tcctcgccgg ctagccaccg atctgagagt cccgagtatg tggatctcaa 600
 taccatgtac aatggaggct gcaacaacat ggcccagaac caacaatacg gaatgattat 660
 ggagcagtct gttgtttcca cagcgcttgc aattccagtg gccttcctc cggcagtgga 720
 ggtcatgggc tcctccaacg tgggcacttg caaaacgatt ccagcctcag cagctccgaa 780
 accgaagcgt agctatacca agaagaacca gccaaagcacc accgccacct ccacaccgac 840
 tgcagctgcg gagtcatctg cctcagtga tctctacacg gaggagttcc agaactttga 900
 ctttgacaac tccgccttgt tcgatgacag cgtcgaggat gacgaggacc tcatgctctt 960
 cagtggcggg gaggacttcg atggcaatga tggatccttt gacttggccg atggtgagaa 1020

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ccaagatgcc gctgccggag gctctggaaa gaagaggcgt ggcaagcaga tcacaccgt 1080
cgtgaagagg aagcgtcgcc tggccgcca tgcacgtgag cgtcgtcgga tgcagaacct 1140
caaccaggcc ttcgatcgtc tccgccagta ccttcctgt ctgggaaacg atcgccagct 1200
gtccaaacac gagaccctcc aaatggccca gacctacata tccgctctcg gggatctgct 1260
gcgctgaatt cccggatccc gatcccagtc ccaagtacta ttctcagtta ttgttgagc 1320
ttgccaaatg ttgtagctac tttgtatata ttgcctggag cccagtagtg aattaccgt 1380
taagtattat gctgtttatt gtttagtta ttagcctaaa tggaagacaa tgattaagac 1440
taaggaagac aaaataaaag caccattaat aatttaa 1477

<210> 64
<211> 312
<212> PRT
<213> DROSOPHILA

<400> 64

Met	Ser	Ser	Ser	Glu	Ile	Tyr	Arg	Tyr	Tyr	Tyr	Lys	Thr	Ser	Glu	Asp	1	5	10	15
Leu	Gln	Gly	Phe	Lys	Thr	Ala	Ala	Ala	Glu	Pro	Tyr	Phe	Asn	Pro	Met	20	25	30	
Ala	Ala	Tyr	Asn	Pro	Gly	Val	Thr	His	Tyr	Gln	Phe	Asn	Gly	Asn	Thr	35	40	45	
Leu	Ala	Ser	Ser	Ser	Asn	Tyr	Leu	Ser	Ala	Asn	Gly	Phe	Ile	Ser	Phe	50	55	60	
Glu	Gln	Ala	Ser	Ser	Asp	Gly	Trp	Ile	Ser	Ser	Ser	Pro	Ala	Ser	His	65	70	75	80
Arg	Ser	Glu	Ser	Pro	Glu	Tyr	Val	Asp	Leu	Asn	Thr	Met	Tyr	Asn	Gly	85	90	95	
Gly	Cys	Asn	Asn	Met	Ala	Gln	Asn	Gln	Gln	Tyr	Gly	Met	Ile	Met	Glu	100	105	110	
Gln	Ser	Val	Val	Ser	Thr	Ala	Pro	Ala	Ile	Pro	Val	Ala	Ser	Pro	Pro	115	120	125	
Ala	Val	Glu	Val	Met	Gly	Ser	Ser	Asn	Val	Gly	Thr	Cys	Lys	Thr	Ile	130	135	140	
Pro	Ala	Ser	Ala	Ala	Pro	Lys	Pro	Lys	Arg	Ser	Tyr	Thr	Lys	Lys	Asn	145	150	155	160
Gln	Pro	Ser	Thr	Thr	Ala	Thr	Ser	Thr	Pro	Thr	Ala	Ala	Ala	Glu	Ser	165	170	175	
Ser	Ala	Ser	Val	Asn	Leu	Tyr	Thr	Glu	Glu	Phe	Gln	Asn	Phe	Asp	Phe	180	185	190	

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Asp Asn Ser Ala Leu Phe Asp Asp Ser Val Glu Asp Asp Glu Asp Leu
 195 200 205
 Met Leu Phe Ser Gly Gly Glu Asp Phe Asp Gly Asn Asp Gly Ser Phe
 210 215 220
 Asp Leu Ala Asp Gly Glu Asn Gln Asp Ala Ala Ala Gly Gly Ser Gly
 225 230 235 240
 Lys Lys Arg Arg Gly Lys Gln Ile Thr Pro Val Val Lys Arg Lys Arg
 245 250 255
 Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met Gln Asn Leu Asn
 260 265 270
 Gln Ala Phe Asp Arg Leu Arg Gln Tyr Leu Pro Cys Leu Gly Asn Asp
 275 280 285
 Arg Gln Leu Ser Lys His Glu Thr Leu Gln Met Ala Gln Thr Tyr Ile
 290 295 300
 Ser Ala Leu Gly Asp Leu Leu Arg
 305 310

<210> 65
 <211> 907
 <212> DNA
 <213> FROG

<400> 65
 gccccggggc cactctgcgc acttgctcggg acttattcgc atttacctgt catggcccgt 60
 ctgctacacg gcgctgctac tgccgctgac tgggtgcgagc tgaaggagct tccatccgag 120
 gccgggctct tggccagaga ttacctacta gacagcagcg acccccgcgc ctggctctcc 180
 gccacttccc tgcaaagtgc ccctgagtac gtgctgcacc ccccggggccg ggccggggcgc 240
 acaaggtgcg ggaactgtgc aaactgaagg ggctgcggga tgatgatgat gatgaggagg 300
 atgatgagga ggaggaagag agatccgagg ggctgtgcag acacaggggt cccctggca 360
 agggccctgg tggggttcag aagcagagga gactggcagc caatgccagg gagaggagga 420
 ggatgcacgg gctcaatcat gccttcgatc agctccgtaa tgtcatccct tccttcaata 480
 acgacaagaa actctccaaa tacgagacct tgcagatggc tcagatctac atcaacgccc 540
 tgtccgacct gctgcaggcg cccccgact ccagagatcc cccctgcccg cccacctacc 600
 aactgcattc ggggccagag cccaggttag tccagtctgg cagcatgaga ttctcggaga 660
 cttccccccg acagtcccc ctcagccaat tccaggaggg agctgctccc agaagggaat 720
 aggatctggg cccatcttca tcttctcggg aagacatcgc ccatcttcat cttcggggag 780
 aagacagcaa gacatcgcaa gatctcatcg gactgacggc gaattccggt ctccctatag 840
 tgagtcgtat taatttcgat aagccagctg cattaatgaa tcggccaaac gcgcggggag 900
 aggcggt 907

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<210> 66
<211> 259
<212> PRT
<213> FROG

<400> 66

Met Ala Arg Leu Leu His Gly Ala Ala Thr Ala Ala Asp Trp Cys Glu
1 5 10 15

Leu Lys Glu Leu Pro Ser Glu Ala Gly Leu Leu Ala Arg Asp Tyr Leu
20 25 30

Leu Asp Ser Ser Asp Pro Arg Ala Trp Leu Ser Ala Thr Ser Leu Gln
35 40 45

Ser Arg Pro Glu Tyr Val Leu His Pro Pro Gly Arg Ala His Lys Val
50 55 60

Arg Glu Leu Cys Lys Leu Lys Gly Leu Arg Asp Asp Asp Asp Asp Glu
65 70 75 80

Glu Glu Asp Asp Glu Glu Glu Glu Glu Arg Ser Glu Gly Leu Cys Arg
85 90 95

His Arg Gly Pro Pro Gly Lys Gly Pro Gly Gly Val Gln Lys Gln Arg
100 105 110

Arg Leu Ala Ala Asn Ala Arg Glu Arg Arg Arg Met His Gly Leu Asn
115 120 125

His Ala Phe Asp Gln Leu Arg Asn Val Ile Pro Ser Phe Asn Asn Asp
130 135 140

Lys Lys Leu Ser Lys Tyr Glu Thr Leu Gln Met Ala Gln Ile Tyr Ile
145 150 155 160

Asn Ala Leu Ser Asp Leu Leu Gln Ala Pro Pro Asp Ser Arg Asp Pro
165 170 175

Pro Cys Pro Pro Thr Tyr Gln Leu His Ser Gly Pro Glu Pro Arg Leu
180 185 190

Val Gln Ser Gly Ser Cys Met Arg Phe Ser Gly Asp Phe Pro Gly Gln
195 200 205

Ser Pro Leu Ser Phe Gln Phe Gln Glu Gly Ala Ala Leu Ser Gly Lys
210 215 220

Gly Ile Gly Ser Ala Pro Ser Ser Ser Ser Gly Glu Asp Ser Lys Thr
225 230 235 240

Ser Pro Arg Ser His Arg Ser Asp Gly Glu Phe Arg Ser Pro Tyr Ser
245 250 255

Glu Ser Tyr

<210> 67

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<211> 19
<212> DNA
<213> SYNTHETIC CONSTRUCT

<400> 67
tgaagctttt ggctttgag 19

<210> 68
<211> 19
<212> DNA
<213> SYNTHETIC CONSTRUCT

<400> 68
ccgctgccaa attctttgg 19

<210> 69
<211> 37
<212> DNA
<213> HUMAN

<400> 69
gggggcactg acagtaatgc atgccgtatt cgaagtt 37

209080" FEB08660